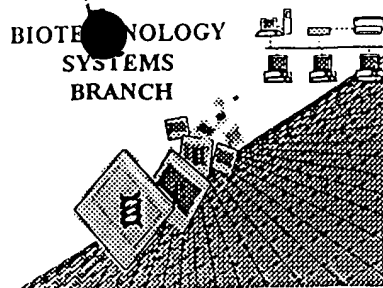


RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/756,070
Source: OIPE
Date Processed by STIC: 7/12/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/756,070

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- | | | |
|----|--|--|
| 1 | _____ Wrapped Nucleics
_____ Wrapped Aminos | The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping." |
| 2 | _____ Invalid Line Length | The rules require that a line not exceed 72 characters in length. This includes white spaces. |
| 3 | _____ Misaligned Amino
_____ Numbering | The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters , instead. |
| 4 | _____ Non-ASCII | The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text . |
| 5 | _____ Variable Length | Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing. |
| 6 | _____ PatentIn 2.0
_____ "bug" | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences. |
| 7 | _____ Skipped Sequences
(OLD RULES) | Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences. |
| 8 | _____ Skipped Sequences
(NEW RULES) | Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000 |
| 9 | _____ Use of n's or Xaa's
(NEW RULES) | Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents. |
| 10 | _____ Invalid <213>
_____ Response | Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence |
| 11 | _____ Use of <220> | Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules) |
| 12 | _____ PatentIn 2.0
_____ "bug" | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk. |

OIPE

RAW SEQUENCE LISTING

DATE: 07/12/2001

PATENT APPLICATION: US/09/756,070

TIME: 09:17:14

Input Set : A:\P-514 sequence list.txt

Output Set: N:\CRF3\07122001\I756070.raw

4 <110> APPLICANT: Paul D. Taylor
 6 <120> TITLE OF INVENTION: DETECTION OF NUCLEIC ACID HETERODUPLEX
 7 MOLECULES BY ANION EXCHANGE CHROMATOGRAPHY
 10 <130> FILE REFERENCE: P-514
 12 <140> CURRENT APPLICATION NUMBER: 09/756,070
 C--> 13 <141> CURRENT FILING DATE: 2001-01-06
 15 <150> PRIOR APPLICATION NUMBER: 60/194,652
 16 <151> PRIOR FILING DATE: 2001-04-04
 18 <150> PRIOR APPLICATION NUMBER: 09/687,834
 19 <151> PRIOR FILING DATE: 2001-10-11
 21 <160> NUMBER OF SEQ ID NOS: 6
 23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 20
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Primer
 30 <220> FEATURE:
 31 <221> NAME/KEY: primer_bind
 32 <222> LOCATION: (1)...(20)
 33 <223> OTHER INFORMATION: Primer
 35 <400> SEQUENCE: 1
 36 aggcactggt cagaatgaag
 38 <210> SEQ ID NO: 2
 39 <211> LENGTH: 20
 40 <212> TYPE: DNA
 41 <213> ORGANISM: Primer
 43 <220> FEATURE:
 44 <221> NAME/KEY: primer_bind
 45 <222> LOCATION: (190)...(209)
 46 <223> OTHER INFORMATION: Primer
 48 <400> SEQUENCE: 2
 49 aatggaaaat acagctcccc
 51 <210> SEQ ID NO: 3
 52 <211> LENGTH: 209
 53 <212> TYPE: DNA
 54 <213> ORGANISM: Homo sapiens
 56 <220> FEATURE:
 57 <221> NAME/KEY: STS
 58 <222> LOCATION: (1)...(209)
 59 <223> OTHER INFORMATION: sY81
 61 <400> SEQUENCE: 3
 62 aggcactggt cagaatgaag tgaatggcac acaggacaag tccagaccca ggaaggtcca 60
 63 gtaacatggg agaagaacgg aaggagttct aaaattcagg gctcccttgg gctcccctgt 120
 64 ttaaaaaatgt aggttttatt attatatttc attgttaaca aaagtccatg agatctgtgg 180
 65 aggataaagg gggagctgta ttttccatt 209
 67 <210> SEQ ID NO: 4
 68 <211> LENGTH: 209

Does Not Comply
Corrected Diskette Needed

See item 10 ERROR
SUMMARY SHEET

20

20

RAW SEQUENCE LISTING

DATE: 07/12/2001

PATENT APPLICATION: US/09/756,070

TIME: 09:17:14

Input Set : A:\P-514 sequence list.txt

Output Set: N:\CRF3\07122001\I756070.raw

```
69 <212> TYPE: DNA
70 <213> ORGANISM: Homo sapiens
72 <220> FEATURE:
73 <221> NAME/KEY: STS
74 <222> LOCATION: (1)...(209)
75 <223> OTHER INFORMATION: sY81
77 <400> SEQUENCE: 4
78 aggcactggt cagaatgaag tgaatggcac acaggacaag tccagaccca ggaaggtcca 60
79 gtaacatggg agaagaacgg aaggagttct aaaattcagg gctcccttgg gctcccctgt 120
80 ttaaaaaatgt aggttttatt attatatttc attgttaaca aaagtccgtg agatctgtgg 180
81 aggataaagg gggagctgta ttttccatt 209
83 <210> SEQ ID NO: 5
84 <211> LENGTH: 209
85 <212> TYPE: DNA
86 <213> ORGANISM: Homo sapiens
88 <220> FEATURE:
89 <221> NAME/KEY: STS
90 <222> LOCATION: (1)...(209)
91 <223> OTHER INFORMATION: sY81
93 <400> SEQUENCE: 5
94 aatggaaaat acagctcccc ctttatcctc cacagatctc atggactttt gttaacaatg 60
95 aaatataata ataaaaccta cattttttaa caggggagcc caaggagcc ctgaatttta 120
96 gaactccttc cgttcttctc ccatgttact ggaccttctt gggctctggac ttgtcctgtg 180
97 tgccattcac ttcattctga ccagtgcct 209
99 <210> SEQ ID NO: 6
100 <211> LENGTH: 209
101 <212> TYPE: DNA
102 <213> ORGANISM: Homo sapiens
104 <220> FEATURE:
105 <221> NAME/KEY: STS
106 <222> LOCATION: (1)...(209)
107 <223> OTHER INFORMATION: sY81
109 <400> SEQUENCE: 6
110 aatggaaaat acagctcccc ctttatcctc cacagatctc acggactttt gttaacaatg 60
111 aaatataata ataaaaccta cattttttaa caggggagcc caaggagcc ctgaatttta 120
112 gaactccttc cgttcttctc ccatgttact ggaccttctt gggctctggac ttgtcctgtg 180
113 tgccattcac ttcattctga ccagtgcct 209
```

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/756,070

DATE: 07/12/2001

TIME: 09:17:15

Input Set : A:\P-514 sequence list.txt

Output Set: N:\CRF3\07122001\I756070.raw

✓ L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date